Sequence Listing

<110> APROGEN INC.

<120> HUMANIZED ANTIBODY AND PROCESS FOR PREPARING SAME

<130> PCA30215/APG

<150> KR10-2002-0015708
<151> 2002-03-22

<160> 38

<170> KopatentIn 1.71

<210> 1
<211> 345
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<220>
<223> HEAVY CHAIN of HZVII

<400> 1
caggtccagc tggtgcagtc tggagctgaa gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaaag cttctggcta caccttcacc agtgcttgga tgaactgggt gcgacaggcc 120

cctggacagg gtcttgagtg gatgggacgg atttatccta gtggtggaag cactagctac 180

gcacagaagt tccagggcag agtcacaatg actgcagaca aatccacgag cacagtctac 240

atggagctca gcagcctgag atctgaggac acggcggtgt attactgtgc aagagagtac 300

cgggttgccc gttggggcca aggaactctg gtcactgtct cttca 345

<210> 2
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> HEAVY CHAIN of HZVII

<400> 2
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Ala Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ala
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Tyr Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Tyr Arg Val Ala Arg Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 3
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> LIGHT CHAIN of HZVII

<400> 3
gatatcgtga tgacccaaac tccactttct ttgtcggtta cccctggaca accagcctct 60

atctcttgca agtcaagtca gagcctctta tatagtaatg gaaaaaccta tttgaattgg 120

ttattacaga agccaggcca gcctccacag cgcctaatct atctggtgtc taatcgggac 180

tctggagtcc ctgacaggtt cagtggcagt ggatcaggaa cagattttac actgaaaatc 240

agcagagtgg aggctgagga tgttggagtt tattactgcg tgcaaggtac acattttcct 300

cagacgttcg gtggaggcac caaggtggaa atcaaa 336

<210> 4
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> LIGHT CHAIN of HZVII

<400> 4

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Arg Leu Ile Tyr Leu Val Ser Asn Arg Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Val Gln Gly
85 90 95

Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Ryu94

<400> 5
gagaattcac attcacgatg tacttg 26

<210> 6
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> HUR43-1

<400> 6
ctgctgcagc tggacctgac tctggacacc att 33

<210> 7
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> HUR44-1

<400> 7
caggtccagc tgcagcagtc tggacctgaa ctg 33

<210> 8
<211> 33
<212> DNA
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<220>
<223> HUR45-1

<400> 8
tgggcccttg gtggaggctg cagagacagt gac 33

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> HUR46-1

<400> 9
gcctccacca agggcccatc ggtcttcccc ctg 33

<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> HUR31

<400> 10
cagcggccgc tcatttaccc ggggacag 28

<210> 11
<211> 26
<212> DNA

<213> Artificial Sequence

<220>
<223> Ryu86

<400> 11
caaagcttgg aagcaagatg gattca 26

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> HUR48

<400> 12
caagatatcc ccacaggtac cagatac 27

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> HUR49

<400> 13
tgtggggata tcttgatgac ccaaact 27

<210> 14
<211> 27
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<223> HUR50

<400> 14
cacagatctt ttgatttcca gcttggt 27

<210> 15
<211> 27
<212> DNA
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<223> HUR51

<400> 15
atcaaaagat ctgtggctgc accatct 27

<210> 16
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> CK1D

<400> 16
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<211> 27
<212> DNA
<213> Artificial Sequence

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<223> YM001N

<400> 17
ccggaattca cattcacgat gtacttg 27

<210> 18
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> YM003

<400> 18
tgcccccaga ggtgct 16

<210> 19
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> ym257

<400> 19
acgcattcag tgcttcttgg atgaactggg tga 33

<210> 20
<211> 31
<212> DNA
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<220>
<223> YM258

<400> 20
atccaagaag cactgaatgc gtagccagaa g 31

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> YM004

<400> 21
ccaattcaaa gcggtttttc cattactata taagaggc 38

<210> 22
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> YM009

<400> 22
gcagccaccg tacgtttgat ttccaccttg gt 32

<210> 23
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Ryu 166

<400> 23
ggatttgtct gcagtcattg tggctctgcc ctggaactt 39

<210> 24
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Hur 37

<400> 24
gacaaatcca cgagcacagt ctacatg 27

<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Ryu 118

<400> 25
ctgtggaggc tggcctggct tctgtaataa cca 33

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Ryu 119

<400> 26
ggccagcctc cacagctcct aatctatctg 30

<210> 27
<211> 345
<212> DNA
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<220>
<223> KR127VH

<400> 27
caggtccagc tgcagcagtc tggacctgaa ctggtgaagc ctggggcctc agtgaagatt 60

tcctgcaaag cttctggcta cgcattcagt agttcttgga tgaactgggt gaagcagagg 120

cctggacagg gtcttgagtg gattggacgg atttatcctg gagatggaga tactaactac 180

aatgggaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgtggac tctgcggtct atttctgtgc aagagagtac 300

gacgaggctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 28
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Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Glu Tyr Asp Glu Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 29
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> KR127VK

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atctcttgca agtcaagtca gagcctctta tatagtaatg gaaaaaccta tttgaattgg 120

ttattacaga ggccaggcca gtctccaaag cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggaa cagattttac actgaaaatc 240

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cagacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 30
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> KR127VK

<400> 30

Asp Ile Leu Met Thr Gln Thr Pro Leu Ile Leu Ser Val Thr Ile Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ile Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Val Gln Gly
85 90 95

Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 31
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> DP7

<400> 31
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cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaga 294

<210> 32
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> DP7

<400> 32
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg

<210> 33
<211> 302
<212> DNA
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<220>
<223> DPK12

<400> 33
gatattgtga tgacccagac tccactctct ctgtccgtca cccctggaca gccggcctcc 60

atctcctgca agtctagtca gagcctcctg catagtgatg gaaagaccta tttgtattgg 120

tacctgcaga agccaggcca gcctccacag ctcctgatct atgaagtttc caaccggttc 180

tctggagtgc cagataggtt cagtggcagc gggtcaggga cagatttcac actgaaaatc 240

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cc 302

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<212> PRT
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<220>
<223> DPK12

<400> 34
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
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Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Ile Gln Leu Pro
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<210> 35
<211> 345
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<220>
<223> HEAVY CHAIN of HZI

<400> 35
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tcctgcaaag cttctggcta cgcattcagt agttcttgga tgaactgggt gcgacaggcc 120

cctggacagg gtcttgagtg gattggacgg atttatcctg gagatggaga tactaactac 180

gcacagaagt tccagggcaa ggccacactg actgcagaca aatccacgag cacagcctac 240

atggagctca gcagcctgag atctgaggac acggcggtct atttctgtgc aagagagtac 300

gacgaggctt actggggcca aggaactctg gtcactgtct cttca 345

<210> 36
<211> 115
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<213> Artificial Sequence

<220>
<223> HEAVY CHAIN of HZI

<400> 36
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Tyr Pro Gly Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Glu Tyr Asp Glu Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 37
<211> 336
<212> DNA
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<220>
<223> LIGHT CHAIN of HZI

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atctcttgca agtcaagtca gagcctctta tatagtaatg gaaaaaccta tttgaattgg 120

ttattacaga agccaggcca gtctccaaag cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cagtggcagt ggatcaggaa cagattttac actgaaaatc 240

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cagacgttcg gtggaggcac caaggtggaa atcaaa 336

<210> 38
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<220>
<223> LIGHT CHAIN of HZI

<400> 38

Asp Ile Leu Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
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Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asn Gly Lys Thr Tyr Leu Tyr Trp Leu Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Val Gln Gly
85 90 95

Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110